Phyre$^2$

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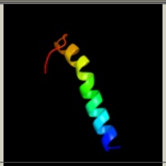
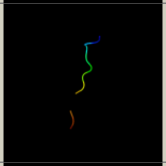
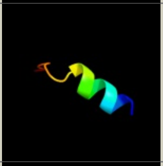
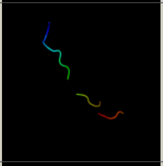
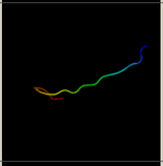
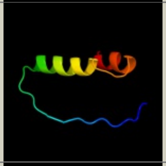
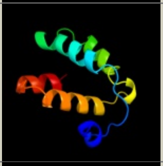
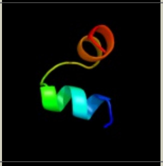
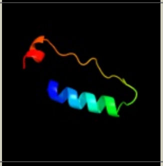
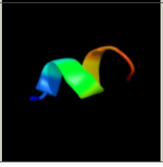
| Description | P46125 |
| Date | Thu Jan 5 12:04:03 GMT 2012 |
| Unique Job ID | c8414c9e288aec28 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2l9uA_ | Alignment |  | 58.6 | 28 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3;<br>**PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain |
| 2 | d2enda_ | Alignment |  | 37.2 | 41 | **Fold:**T4 endonuclease V<br>**Superfamily:**T4 endonuclease V<br>**Family:**T4 endonuclease V |
| 3 | c1i7mD_ | Alignment |  | 21.8 | 46 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**s-adenosylmethionine decarboxylase beta chain;<br>**PDBTitle:** human s-adenosylmethionine decarboxylase with covalently bound2 pyruvoyl group and complexed with 4-amidinoindan-1-one-2'-3 amidinohydrazone |
| 4 | d1nexa2 | Alignment |  | 16.3 | 25 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**BTB/POZ domain |
| 5 | c1msvB_ | Alignment |  | 14.1 | 37 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**s-adenosylmethionine decarboxylase proenzyme;<br>**PDBTitle:** the s68a s-adenosylmethionine decarboxylase proenzyme2 processing mutant. |
| 6 | d1jl0a_ | Alignment |  | 13.3 | 37 | **Fold:**S-adenosylmethionine decarboxylase<br>**Superfamily:**S-adenosylmethionine decarboxylase<br>**Family:**S-adenosylmethionine decarboxylase |
| 7 | c2lm4A_ | Alignment |  | 12.8 | 19 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**succinate dehydrogenase assembly factor 2, mitochondrial;<br>**PDBTitle:** solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a |
| 8 | c1ciiA_ | Alignment |  | 11.7 | 16 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 9 | d1zyba1 | Alignment |  | 10.8 | 33 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**CAP C-terminal domain-like |
| 10 | d1hv2a_ | Alignment |  | 10.0 | 11 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**BTB/POZ domain |
| 11 | d1jb0i_ | Alignment |  | 9.7 | 44 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI<br>**Family:**Subunit VIII of photosystem I reaction centre, PsaI |

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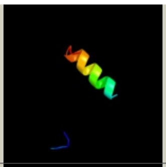
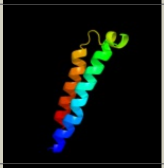
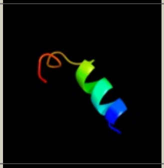
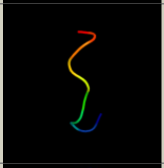
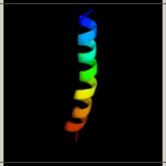
|---|---|---|---|---|---|---|
| 12 | c3h4cA_ | Alignment |  | 8.9 | 30 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor tfiib-like;<br>**PDBTitle:** structure of the c-terminal domain of transcription factor iib from2 trypanosoma brucei |
| 13 | c2gezE_ | Alignment |  | 8.7 | 11 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit;<br>**PDBTitle:** crystal structure of potassium-independent plant asparaginase |
| 14 | c2zjsE_ | Alignment |  | 8.2 | 33 | **PDB header:**protein transport/immune system<br>**Chain:** E: **PDB Molecule:**preprotein translocase sece subunit;<br>**PDBTitle:** crystal structure of secye translocon from thermus thermophilus with a2 fab fragment |
| 15 | d1lgha_ | Alignment |  | 7.6 | 43 | **Fold:**Light-harvesting complex subunits<br>**Superfamily:**Light-harvesting complex subunits<br>**Family:**Light-harvesting complex subunits |
| 16 | d1kf6d_ | Alignment |  | 7.2 | 11 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Fumarate reductase respiratory complex transmembrane subunits<br>**Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD) |
| 17 | d2c9wc1 | Alignment |  | 7.2 | 11 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**BTB/POZ domain |
| 18 | d1rqba1 | Alignment |  | 7.0 | 62 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**post-HMGL domain-like<br>**Family:**Conserved carboxylase domain |
| 19 | c2ifoA_ | Alignment |  | 7.0 | 35 | **PDB header:**virus<br>**Chain:** A: **PDB Molecule:**inovirus;<br>**PDBTitle:** model-building studies of inovirus: genetic variations on a2 geometric theme |
| 20 | c2ksrA_ | Alignment |  | 6.4 | 17 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2;<br>**PDBTitle:** nmr structures of tm domain of the n-acetylcholine receptor b2 subunit |
| 21 | d1q5za_ | Alignment | not modelled | 6.1 | 29 | **Fold:**Invasion protein A (SipA) , C-terminal actin binding domain<br>**Superfamily:**Invasion protein A (SipA) , C-terminal actin binding domain<br>**Family:**Invasion protein A (SipA) , C-terminal actin binding domain |
| 22 | c1q5zA_ | Alignment | not modelled | 6.1 | 29 | **PDB header:**cell invasion<br>**Chain:** A: **PDB Molecule:**sipa;<br>**PDBTitle:** crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa) |
| 23 | d1fs1b2 | Alignment | not modelled | 6.0 | 23 | **Fold:**POZ domain<br>**Superfamily:**POZ domain<br>**Family:**BTB/POZ domain |
| 24 | c3juiA_ | Alignment | not modelled | 5.7 | 21 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon;<br>**PDBTitle:** crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit |
| 25 | c3lw5K_ | Alignment | not modelled | 5.6 | 27 | **PDB header:**photosynthesis<br>**Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak;<br>**PDBTitle:** improved model of plant photosystem i |
| 26 | c2voyB_ | Alignment | not modelled | 5.3 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium<br>**PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus |